RAW SEQUENCE LISTING
ERROR REPORT

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form:

Application Serial Number: *10/624,619*

Source: *QIPE*

Date Processed by STIC: *7/31/2003*

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   APPLICANT, WITH A NOTICE TO COMPLY or,
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A**
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TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
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1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission
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Revised 04/24/2003

OIPE

RAW SEQUENCE LISTING   DATE: 07/31/2003
PATENT APPLICATION: US/10/624,619   TIME: 08:01:13

        Input Set : A:\0875CSEQUENCE LISTING.txt
        Output Set: N:\CRF4\07312003\J624619.raw

   4 <110> APPLICANT: Duvick, Jonathan P.
   5   Gilliam, Jacob T.
   6   Maddox, Joyce R.
   7   Crasta, Oswald R.
   8   Folkerts, Otto
  11 <120> TITLE OF INVENTION: Amino Polyol Amine Oxidase
  12   Polynucleotides and Related Polypeptides and Methods of Use
  15 <130> FILE REFERENCE: 0875C
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/624,619
C--> 17 <141> CURRENT FILING DATE: 2003-07-22
  17 <150> PRIOR APPLICATION NUMBER: US 60/092,936
  18 <151> PRIOR FILING DATE: 1998-07-15
  20 <150> PRIOR APPLICATION NUMBER: US 09/352,168
  21 <151> PRIOR FILING DATE: 1999-07-12
  23 <160> NUMBER OF SEQ ID NOS: 33
  25 <170> SOFTWARE: FastSEQ for Windows Version 3.0

see pp 6-7, too

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

  3641 <210> SEQ ID NO: 32
  3642 <211> LENGTH: 2490
  3643 <212> TYPE: DNA
  3644 <213> ORGANISM: Unknown
  3646 <220> FEATURE: *Per 1.823 of Sequence Rules, 4 lines MAXIMUM*
  3647 <223> OTHER INFORMATION: GST:glyc(-)APAO open reading frame, 2490 nt; GST   *for <223>*
  3648   and linker, nt 1-687; Glyc (-) APAO, nt 688-2490;   *section.*
  3649   mutation in putative glycosylation sites in bold
  3650 /2207/ and underlined, nt 1288-1290 (AAT->TCC) and nt
E-- /223/ 1303-1305 (AGC->AAC) → *move over (Do NOT use TAB codes) insert*
W--> 3653 <221> NAME/KEY: CDS
  3654 <222> LOCATION: (1)...(2487)
W--> 3656 <221> misc_feature
  3657 <222> LOCATION: (1)...(687)
  3658 <223> OTHER INFORMATION: GST and linker
W--> 3660 <221> misc_feature
  3661 <222> LOCATION: (688)...(2490)
  3662 <223> OTHER INFORMATION: Glyc (-) APAO
W--> 3664 <221> mutation
  3665 <222> LOCATION: (1288)...(1290)
  3666 <223> OTHER INFORMATION: mutation in putative glycosylation site (AAT->TCC)
W--> 3668 <221> mutation
  3669 <222> LOCATION: (1303)...(1305)

insert

Insert another <220> after 4th line, and add a <223> to beginning of 5th line

Please edit Seqs. 20 and 30, too.

```
   3670 <223> OTHER INFORMATION: mutation in putative glycosylation site (AGC->AAC)
W-->  3672 <400> 32
   3673  atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc      48
   3674  Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
   3675   1               5                   10                  15
   3677  act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg      96
   3678  Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
   3679               20                  25                  30
   3681  tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg     144
   3682  Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
   3683           35                  40                  45
   3685  ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa     192
   3686  Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
   3687           50                  55                  60
   3689  tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac     240
   3690  Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
   3691   65                  70                  75                  80
   3693  atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa     288
   3694  Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
   3695               85                  90                  95
   3697  gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt     336
   3698  Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
   3699              100                 105                 110
   3701  aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa     384
   3702  Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
   3703              115                 120                 125
   3705  atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat     432
   3706  Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
   3707              130                 135                 140
   3709  ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat     480
   3710  Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
   3711  145                 150                 155                 160
   3713  gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta     528
   3714  Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
   3715              165                 170                 175
   3717  gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac     576
   3718  Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
   3719              180                 185                 190
   3721  ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc     624
   3722  Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
   3723              195                 200                 205
   3725  acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt     672
   3726  Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
   3727              210                 215                 220
   3729  gga tcc ccg gaa ttc atg gca ctt gca ccg agc tac atc aat ccc cca     720
   3730  Gly Ser Pro Glu Phe Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro
   3731  225                 230                 235                 240
   3733  aac gtc gcc tcc cca gca ggg tat tct cac gtc ggc gta ggc cca gac     768
   3734  Asn Val Ala Ser Pro Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp
```

```
3735                   245                   250                   255
3737  gga ggg agg tat gtg aca ata gct gga cag att· gga caa gac gct tcg      816
3738  Gly Gly Arg Tyr Val Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser
3739              260                   265                   270
3741  ggc gtg aca gac cct gcc tac gag aaa cag gtt gcc caa gca ttc gcc      864
3742  Gly Val Thr Asp Pro Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala
3743              275                   280                   285
3745  aat ctg cga gct tgc ctt gct gca gtt gga gcc act tca aac gac gtc      912
3746  Asn Leu Arg Ala Cys Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val
3747          290                   295                   300
3749  acc aag ctc aat tac tac atc gtc gac tac gcc ccg agc aaa ctc acc      960
3750  Thr Lys Leu Asn Tyr Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr
3751  305                   310                   315                   320
3753  gca att gga gat ggg ctg aag gct acc ttt gcc ctt gac agg ctc cct     1008
3754  Ala Ile Gly Asp Gly Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro
3755              325                   330                   335
3757  cct tgc acg ctg gtg cca gtg tcg gcc ttg tct tca cct gaa tac ctc     1056
3758  Pro Cys Thr Leu Val Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu
3759              340                   345                   350
3761  ttt gag gtt gat gcc acg gcg ctg gtg ccg gga cac acg acc cca gac     1104
3762  Phe Glu Val Asp Ala Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp
3763              355                   360                   365
3765  aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag     1152
3766  Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu
3767          370                   375                   380
3769  acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag     1200
3770  Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu
3771  385                   390                   395                   400
3773  gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc     1248
3774  Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro
3775              405                   410                   415
3777  ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc tcg gac agc     1296
3778  Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Ser Asp Ser
3779              420                   425                   430
3781  aac caa aac gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc     1344
3782  Asn Gln Asn Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly
3783              435                   440                   445
3785  gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt     1392
3786  Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly
3787          450                   455                   460
3789  aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt     1440
3790  Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val
3791  465                   470                   475                   480
3793  gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa     1488
3794  Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu
3795              485                   490                   495
3797  gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc     1536
3798  Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu
3799              500                   505                   510
```

RAW SEQUENCE LISTING   DATE: 07/31/2003
PATENT APPLICATION: US/10/624,619   TIME: 08:01:13

Input Set : A:\0875CSEQUENCE LISTING.txt
Output Set: N:\CRF4\07312003\J624619.raw

```
3801  gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct    1584
3802  Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro
3803          515              520               525
3805  gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg    1632
3806  Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val
3807          530              535               540
3809  gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt    1680
3810  Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser
3811  545              550               555               560
3813  gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag    1728
3814  Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln
3815              565               570               575
3817  tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca    1776
3818  Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser
3819              580               585               590
3821  aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa    1824
3822  Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu
3823          595               600               605
3825  att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc    1872
3826  Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala
3827          610               615               620
3829  gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat    1920
3830  Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr
3831  625              630               635               640
3833  ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg    1968
3834  Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu
3835              645               650               655
3837  gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg    2016
3838  Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp
3839              660               665               670
3841  gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg    2064
3842  Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser
3843          675               680               685
3845  agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat    2112
3846  Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp
3847          690               695               700
3849  cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag    2160
3850  Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys
3851  705              710               715               720
3853  tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa    2208
3854  Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln
3855              725               730               735
3857  ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc    2256
3858  Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala
3859              740               745               750
3861  aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct    2304
3862  Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala
3863              755               760               765
3865  ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg    2352
```

```
3866   Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala
3867       770             775             780
3869   ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct      2400
3870   Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser
3871   785             790             795             800
3873   tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga      2448
3874   Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg
3875               805             810             815
3877   ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag            2490
3878   Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
3879               820             825
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/31/2003

PATENT APPLICATION: **US/10/624,619**   TIME: 08:01:14

Input Set : **A:\0875CSEQUENCE LISTING.txt**

Output Set: **N:\CRF4\07312003\J624619.raw**

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"

or"Unknown". Please explain source of genetic material in <220> to <223>

section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)

(Sec.1.823 of new Rules)

Seq#: ~~19, 29, 24,~~ (25) ~~26~~ (27) ~~28~~ (29) ~~30~~ (31) ~~32~~ (33)

see p. 7 for example

10/624,619 ?

```
<210> 25
<211> 1000
<212> PRT
<213> Unknown        ) no explanation given

<220>
<221> SIGNAL
<222> (1)...(24)

<400> 25
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Input Set : **A:\0875CSEQUENCE LISTING.txt**
Output Set: **N:\CRF4\07312003\J624619.raw**

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L:17 M:270 C: Current Application Number differs, Replaced Current Application No
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:43 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:300
L:284 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:287 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:552 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:799 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:1041 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:1045 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:1049 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:1340 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:1347 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1348 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1350 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:1354 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:1813 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1817 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:1821 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:1825 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:1829 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:1832 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:1836 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:2099 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>
ORGANISM:Unknown
L:2099 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:2099
L:2237 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:2241 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:2245 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:2249 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:2253 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:2256 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:2260 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:2520 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
ORGANISM:Unknown
L:2520 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:2520
L:2657 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:2660 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:2664 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:2668 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:2672 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:2676 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:2680 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:2991 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:29, <213>
ORGANISM:Unknown
L:2991 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>
ORGANISM:Unknown
L:2991 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:2991
L:3155 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3156 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3158 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3162 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:3166 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
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Input Set : **A:\0875CSEQUENCE LISTING.txt**
Output Set: **N:\CRF4\07312003\J624619.raw**

L:3170 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:3174 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:3177 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:3181 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:3488 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:31, <213>
ORGANISM:Unknown
L:3488 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>
ORGANISM:Unknown
L:3488 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:3488
L:3651 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:3653 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3656 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3660 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3664 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3668 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3672 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3887 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:33, <213>
ORGANISM:Unknown